AMENDMENT

In the Claims:

Please cancel claim 13.

Please amend claims 1, 4, 11, 12, 14, 15, 17, 21, 22, 25, and 26 as follows:

1. [Thrice Amended] A method of making a mixture of variable number tandem repeat (VNTR) alleles and their flanking regions of the genomic DNA of one or more members of a species of interest, which method comprises the steps of:

a) dividing genomic DNA of the species of interest into fragments,

b) ligating to each end of each fragment an adapter thereby forming a mixture of adaptor-terminated fragments in which each 3'-end is blocked to prevent enzymatic chain extension,

c) contacting a portion of the mixture of adaptor-terminated fragments with an adaptor primer and a VNTR primer wherein said portion of the mixture of adaptor terminated fragments serves as a template to create a mixture of 5'-flanking VNTR amplimers;

d) contacting a portion of the mixture of adaptor-terminated fragments with an adaptor primer and a VNTR antisense primer wherein said portion of the mixture of adaptor-terminated fragments serves as template to create a mixture of 3'-flanking VNTR amplimers,

e) and producing a desired mixture of VNTR alleles and their flanking regions by contacting genomic DNA of the one or more members of the species of interest with the mixture of 5'-flanking VNTR amplimers and/or the mixture of 3'-flanking VNTR amplimers as primers wherein said genomic DNA of the one or more members of the species of interest is used as template.

4. [Amended] The method of claim 1, wherein in step c) and/or d) at least one adaptor or primer used contains at least one phosphorothioate bond.

11. [Twice Amended] A mixture of one or more VNTR alleles and their flanking regions, said mixture consisting essentially of a representative mixture of alleles of a chosen variable number tandem repeat (VNTR) sequence and their flanking regions on both sides, wherein each member of the representative misture of alleses has an adaptor at each of its 3'-end and its 5'-end.

12. [Amended] The mixture of one or more VNTR alleles and their flanking regions of claim 11, wherein the mixture of alleles is representative of those which manifest a trait of interest.

14. [Twice Amended] A composition consisting essentially of one or more copies of a single variable number tandem repeat (VNTR) allele and its flanking regions and an adaptor at each of its 3'-end and its 5'-end, said allele being characteristic of those which manifest a trait of interest.

15. [Twice Amended] A mixture of VNTR flanking sequences, said mixture consisting essentially of a representative mixture of 3'-flanking regions of a chosen variable number tandem repeat (VNTR) sequence, each member of the mixture carrying an adaptor at its 3'-end, and a representative mixture of 5'-flanking regions of a chosen VNTR sequence, each member of the mixture carrying the same adaptor at its 5'-end.

17. [Once Amended] The method of claim 16, wherein the mixture of polymorphic alleles is a mixture of alleles of a chosen variable number tandem repeat (VNTR) sequence and their flanking regions.

21. [Thrice Amended] A method of making a mixture of amplimers which method comprises the steps of:

a) dividing genomic DNA of one or more members of a species of interest into fragments,

b) ligating to each end of each fragment an adaptor thereby forming a mixture of adaptor-terminated fragments in which each 3'-end is blocked to prevent enzymatic chain extension, and

c) contacting a portion of the mixture of adaptor-terminated fragments with an adaptor primer and a variable number tandem repeat (VNTR) primer wherein said portion of the mixture of adaptor-terminated fragments serves as a template to create a mixture of 5'-flanking VNTR amplimers, and/or

d) contacting a portion of the mixture of adaptor-terminated fragments with an adaptor primer and a VNTR antisense primer wherein said portion of the mixture of adaptor-terminated fragments serves as a template to create a mixture of 3'-flanking VNTR amplimers

22. [Twice Amended] A method of identifying an allele which is linked to a trait of interest, which method comprises incubating together under hybridisation conditions: a composition consisting essentially of molecules of nucleic acid containing a polymorphic allele and its flanking sequences representative of those which manifest the trait of interest; and a mixture of molecules of nucleic acid which contain

polymorphic alleles and their flanking sequences representative and derived from more than one of those which do not manifest the trait of interest; and selecting at least one match and/or at least one mis-match to provide at least one allele or fragment thereof which is linked to the trait of interest.

25. [Thrice Amended] A method for diagnosing a trait of interest comprising the step of identifying an allele which is linked to a trait of interest according to the method of claim 22, wherein said molecules of nucleic acid are contacted with a composition consisting essentially of one or more copies of a single VNTR allele and its flanking regions and an adaptor at each of its 3'-end and its 5'-end, said allele being characteristic of those which manifest a trait of interest.

26. [Amended] The method of claim 1 or claim 16, wherein the VNTR allele and its flanking regions, or the mixture of VNTR alleles and their flanking regions, is analysed by being applied under hybridisation conditions to an array of immobilised VNTR alleles and/or their flanking regions.